

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/693,316  
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IFWO

## RAW SEQUENCE LISTING

DATE: 12/11/2006

PATENT APPLICATION: US/10/693,316

TIME: 11:55:05

Input Set : N:\Crif3\RULE60\10693316.raw

Output Set: N:\CRF4\12112006\J693316.raw

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1 <110> APPLICANT: Lee, Arthur M.E.
2     Jain, Mukesh
3     Watanabe, Masafumi
4 <120> TITLE OF INVENTION: IN VITRO DIFFERENTIATION OF VASCULAR SMOOTH MUSCLE
5     CELLS AND REAGENTS RELATED THERETO
6 <130> FILE REFERENCE: APV-382.01
7 <140> CURRENT APPLICATION NUMBER: US/10/693,316
8 <141> CURRENT FILING DATE: 2003-10-23
9 <150> PRIOR APPLICATION NUMBER: US/09/181,311
10 <151> PRIOR FILING DATE: 1998-10-28
11 <150> PRIOR APPLICATION NUMBER: 60/063,363
12 <151> PRIOR FILING DATE: 1997-10-28
13 <150> PRIOR APPLICATION NUMBER: 60/080,420
14 <151> PRIOR FILING DATE: 1998-04-02
15 <150> PRIOR APPLICATION NUMBER: 60/096,685
16 <151> PRIOR FILING DATE: 1998-08-14
17 <160> NUMBER OF SEQ ID NOS: 23
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 153
22 <212> TYPE: DNA
23 <213> ORGANISM: Murine
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Clone WO11
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28     gccgatgaga accaggagta cagcccatg actgggcagt gtcgctctcg ggtcacggaa 120
29     gattcagggtg tggatcgtca gcctaggcga aga 153
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 143
33 <212> TYPE: DNA
34 <213> ORGANISM: Rattus
35 <220> FEATURE:
36 <223> OTHER INFORMATION: Clone LTBP-1
37 <400> SEQUENCE: 2
38     agtgggtgtat gtggggaggc tttctgtgaa aatgtggaag ggtccttcct gtgcgtgtgt 60
39     gccgatgaga accaggagta cagcccatg actgggcagt gtcgctcccg ggctactgaa 120
40     gattcagggtg tggatcgtca gcc 143
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 1128
44 <212> TYPE: PRT
45 <213> ORGANISM: Homo sapiens
46 <220> FEATURE:

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47 &lt;223&gt; OTHER INFORMATION: ACLP

48 &lt;400&gt; SEQUENCE: 3

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49 Met Ala Ala Val Arg Gly Ala Pro Leu Leu Ser Cys Leu Leu Ala Leu
50 1 5 10 15
51 Leu Ala Leu Cys Pro Gly Gly Arg Pro Gln Thr Val Leu Thr Asp Asp
52 20 25 30
53 Glu Ile Glu Glu Phe Leu Glu Gly Phe Leu Ser Glu Leu Glu Pro Glu
54 35 40 45
55 Pro Arg Glu Asp Asp Val Glu Ala Pro Pro Pro Pro Glu Pro Thr Pro
56 50 55 60
57 Arg Val Arg Lys Ala Gln Ala Gly Gly Lys Pro Gly Pro Gly Thr Ala
58 65 70 75 80
59 Ala Glu Val Pro Pro Glu Lys Thr Lys Asp Lys Gly Lys Lys Gly Lys
60 85 90 95
61 Lys Asp Lys Gly Pro Lys Val Pro Lys Glu Ser Leu Glu Gly Ser Pro
62 100 105 110
63 Arg Pro Pro Lys Lys Gly Lys Glu Lys Pro Pro Lys Ala Thr Lys Lys
64 115 120 125
65 Pro Lys Glu Lys Pro Pro Lys Ala Thr Lys Lys Pro Lys Glu Glu Pro
66 130 135 140
67 Pro Lys Ala Thr Lys Lys Pro Lys Glu Lys Lys Ala Thr Lys Lys Pro
68 145 150 155 160
69 Pro Ser Gly Lys Arg Pro Pro Ile Leu Ala Pro Ser Glu Thr Leu Glu
70 165 170 175
71 Trp Pro Leu Pro Pro Pro Pro Ser Pro Gly Pro Glu Glu Leu Pro Gln
72 180 185 190
73 Glu Gly Gly Ala Pro Leu Ser Asn Asn Trp Gln Asn Pro Gly Glu Glu
74 195 200 205
75 Thr His Val Glu Ala Gln Glu His Gln Pro Glu Pro Glu Glu Glu Thr
76 210 215 220
77 Glu Gln Pro Thr Leu Asp Tyr Asn Ile Glu Arg Glu Asp Tyr Glu Asp
78 225 230 235 240
79 Phe Glu Tyr Ile Arg Arg Gln Lys Gln Pro Arg Pro Pro Pro Ser Arg
80 245 250 255
81 Arg Arg Arg Pro Glu Arg Val Trp Pro Glu Pro Pro Glu Glu Lys Ala
82 260 265 270
83 Pro Ala Pro Ala Pro Glu Glu Arg Ile Glu Pro Pro Val Lys Pro Leu
84 275 280 285
85 Leu Pro Pro Leu Pro Pro Asp Tyr Gly Asp Gly Tyr Val Ile Pro Asn
86 290 295 300
87 Tyr Asp Asp Met Asp Tyr Gly Pro Pro Pro Pro Gln Lys Pro Asp Ala
88 305 310 315 320
89 Glu Arg Gln Thr Asp Glu Glu Lys Glu Glu Lys Lys Pro Lys Lys
90 325 330 335
91 Glu Asp Ser Ser Pro Lys Glu Glu Thr Asp Lys Trp Ala Val Glu Lys
92 340 345 350
93 Gly Lys Asp His Lys Glu Pro Arg Lys Gly Glu Glu Leu Glu Glu Glu
94 355 360 365
95 Trp Thr Pro Thr Glu Lys Val Lys Cys Pro Pro Ile Gly Met Glu Ser

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96          370          375          380
97 His Arg Ile Asn Gln Ile Arg Ala Ser Ser Met Leu Arg His Gly Leu
98 385          390          395          400
99 Gly Ala Gln Arg Gly Arg Leu Asn Met Gln Thr Gly Ala Thr Glu Asp
100          405          410          415
101 Asp Tyr Tyr Asp Gly Ala Trp Cys Ala Glu Asp Asp Ala Arg Thr Gln
102          420          425          430
103 Trp Ile Glu Val Asp Thr Arg Arg Thr Thr Arg Phe Thr Gly Val Ile
104          435          440          445
105 Thr Gln Gly Arg Asp Ser Ser Ile His Asp Asp Phe Val Thr Thr Phe
106          450          455          460
107 Phe Phe Ser Asn Asp Ser Gln Thr Trp Val Met Tyr Thr Asn Gly Tyr
108          465          470          475          480
109 Glu Glu Met Thr Phe His Gly Asn Val Asp Lys Asp Thr Pro Val Leu
110          485          490          495
111 Ser Glu Leu Pro Glu Pro Val Val Ala Arg Phe Ile Arg Ile Tyr Pro
112          500          505          510
113 Leu Thr Trp Asn Gly Ser Leu Cys Met Arg Leu Glu Val Leu Gly Cys
114          515          520          525
115 Ser Val Ala Pro Val Tyr Ser Tyr Tyr Ala Gln Asn Glu Val Val Asp
116          530          535          540
117 Asp Leu Asp Phe Arg His His Ser Tyr Lys Asp Met Arg Gln Leu Met
118          545          550          555          560
119 Lys Val Val Asn Glu Glu Cys Pro Thr Ile Thr Arg Thr Tyr Ser Leu
120          565          570          575
121 Gly Lys Ser Ser Arg Gly Leu Lys Ile Tyr Ala Met Glu Ile Ser Asp
122          580          585          590
123 Asn Pro Gly Glu His Glu Leu Gly Glu Pro Glu Phe Arg Tyr Thr Ala
124          595          600          605
125 Gly Ile His Gly Asn Glu Val Leu Gly Arg Glu Leu Ile Leu Met Gln
126          610          615          620
127 Tyr Leu Cys Arg Glu Tyr Arg Asp Gly Asn Pro Arg Val Arg Ser Leu
128          625          630          635          640
129 Val Gln Asp Thr Arg Ile His Leu Val Pro Ser Leu Asn Pro Asp Gly
130          645          650          655
131 Tyr Glu Val Ala Ala Gln Met Gly Ser Glu Phe Gly Asn Trp Ala Leu
132          660          665          670
133 Gly Leu Trp Thr Glu Glu Gly Phe Asp Ile Phe Glu Asp Phe Pro Asp
134          675          680          685
135 Leu Asn Ser Val Leu Trp Gly Ala Glu Glu Phe Val Pro Tyr Arg Val
136          690          695          700
137 Pro Asn Asn Asn Leu Pro Ile Pro Glu Arg Tyr Leu Ser Pro Asp Ala
138          705          710          715          720
139 Thr Val Ser Thr Glu Val Arg Ala Ile Ile Ala Trp Met Glu Lys Asn
140          725          730          735
141 Pro Phe Val Leu Gly Ala Asn Leu Asn Gly Gly Glu Arg Leu Val Ser
142          740          745          750
143 Tyr Pro Tyr Asp Met Ala Arg Thr Pro Thr Gln Glu Gln Leu Leu Ala
144          755          760          765

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145   Ala Ala Met Ala Ala Ala Glu Gly Glu Asp Glu Val Ser Glu Ala Gln
146       770               775               780
147   Glu Thr Pro Asp His Ala Ile Phe Arg Trp Leu Ala Ile Ser Phe Ala
148       785               790               795               800
149   Ser Ala His Leu Thr Leu Thr Glu Pro Tyr Arg Gly Gly Cys Gln Ala
150               805               810               815
151   Gln Asp Tyr Thr Gly Gly Met Gly Ile Val Asn Gly Ala Lys Trp Asn
152               820               825               830
153   Pro Arg Thr Gly Thr Ile Asn Asp Phe Ser Tyr Leu His Thr Asn Cys
154               835               840               845
155   Leu Glu Leu Ser Phe Tyr Ile Asp Lys Phe Pro His Glu Ser Glu Leu
156       850               855               860
157   Pro Arg Glu Trp Glu Asn Asn Lys Glu Ala Leu Leu Thr Phe Met Glu
158       865               870               875               880
159   Gln Val His Arg Gly Ile Lys Gly Val Val Thr Asp Glu Gln Gly Ile
160               885               890               895
161   Pro Ile Ala Asn Ala Thr Ile Ser Val Ser Gly Ile Asn His Gly Val
162               900               905               910
163   Lys Thr Ala Ser Gly Gly Asp Tyr Trp Arg Ile Leu Asn Pro Gly Glu
164       915               920               925
165   Tyr Arg Val Thr Ala Glu Gly Tyr Thr Pro Ser Ala Lys Thr Cys Asn
166       930               935               940
167   Val Asp Tyr Asp Ile Gly Ala Thr Gln Cys Asn Phe Ile Leu Ala Arg
168       945               950               955               960
169   Ser Asn Trp Lys Arg Ile Arg Glu Ile Met Ala Met Asn Gly Asn Arg
170               965               970               975
171   Pro Ile Pro His Ile Asp Pro Ser Arg Pro Met Thr Pro Gln Gln Arg
172               980               985               990
173   Arg Leu Gln Gln Arg Arg Leu Gln His Arg Leu Arg Leu Arg Ala Gln
174       995               1000               1005
175   Met Arg Leu Asn Ala Thr Thr Thr Leu Gly Pro His Thr Val Pro Pro
176       1010               1015               1020
177   Thr Leu Pro Pro Ala Pro Ala Thr Thr Leu Ser Thr Thr Ile Glu Pro
178       1025               1030               1035               1040
179   Trp Gly Leu Ile Pro Pro Thr Thr Ala Gly Trp Glu Glu Ser Glu Thr
180               1045               1050               1055
181   Glu Thr Tyr Thr Glu Val Val Thr Glu Phe Gly Thr Glu Val Glu Pro
182               1060               1065               1070
183   Glu Phe Gly Thr Lys Val Glu Pro Glu Phe Glu Thr Gln Leu Phe Glu
184       1075               1080               1085
185   Thr Gln Leu Glu Pro Glu Phe Glu Glu Glu Glu Glu Glu Lys Glu
186       1090               1095               1100
187   Glu Glu Ile Ala Thr Gly Gln Ala Phe Pro Phe Thr Thr Val Glu Thr
188       1105               1110               1115               1120
189   Tyr Thr Val Asn Phe Gly Asp Phe
190               1125
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 1102
194 <212> TYPE: PRT

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195 &lt;213&gt; ORGANISM: Murine

196 &lt;220&gt; FEATURE:

197 &lt;223&gt; OTHER INFORMATION: ACLP

198 &lt;400&gt; SEQUENCE: 4

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199      Met Ala Pro Val Arg Thr Ala Ser Leu Leu Cys Gly Leu Leu Ala Leu
200          1          5          10          15
201      Leu Thr Leu Cys Pro Glu Gly Asn Pro Gln Thr Val Leu Thr Asp Asp
202          20          25          30
203      Glu Ile Glu Glu Phe Leu Glu Gly Phe Leu Ser Glu Leu Glu Thr Gln
204          35          40          45
205      Ser Pro Pro Arg Glu Asp Asp Val Glu Val Gln Pro Leu Pro Glu Pro
206          50          55          60
207      Thr Gln Arg Pro Arg Lys Ser Lys Ala Gly Gly Lys Gln Arg Ala Asp
208          65          70          75          80
209      Val Glu Val Pro Pro Glu Lys Asn Lys Asp Lys Glu Lys Lys Gly Lys
210          85          90          95
211      Lys Asp Lys Gly Pro Lys Ala Thr Lys Pro Leu Glu Gly Ser Thr Arg
212          100         105         110
213      Pro Thr Lys Lys Pro Lys Glu Lys Pro Pro Lys Ala Thr Lys Lys Pro
214          115         120         125
215      Lys Glu Lys Pro Pro Lys Ala Thr Lys Lys Pro Lys Glu Lys Pro Pro
216          130         135         140
217      Lys Ala Thr Lys Lys Pro Lys Glu Lys Lys Ala Thr Lys Arg Pro Ser
218          145         150         155         160
219      Ala Gly Lys Lys Phe Ser Thr Val Ala Pro Leu Glu Thr Leu Asp Arg
220          165         170         175
221      Leu Leu Pro Ser Pro Ser Asn Pro Ser Ala Gln Glu Leu Pro Gln Lys
222          180         185         190
223      Arg Asp Thr Pro Phe Pro Asn Ala Trp Gln Gly Gln Gly Glu Glu Thr
224          195         200         205
225      Gln Val Glu Ala Lys Gln Pro Arg Pro Glu Pro Glu Glu Glu Thr Glu
226          210         215         220
227      Met Pro Thr Leu Asp Tyr Asn Ile Glu Lys Glu Asp Tyr Glu Asp Phe
228          225         230         235         240
229      Glu Tyr Ile Arg Arg Gln Lys Gln Pro Arg Pro Thr Pro Ser Arg Arg
230          245         250         255
231      Arg Leu Trp Pro Glu Arg Pro Glu Glu Lys Thr Glu Glu Pro Glu Glu
232          260         265         270
233      Arg Lys Glu Val Glu Pro Pro Leu Lys Pro Leu Leu Pro Pro Asp Tyr
234          275         280         285
235      Gly Asp Ser Tyr Val Ile Pro Asn Tyr Asp Asp Leu Asp Tyr Pro His
236          290         295         300
237      Pro Pro Pro Gln Lys Pro Asp Val Gly Gln Glu Val Asp Glu Glu Lys
238          305         310         315         320
239      Glu Glu Met Lys Lys Pro Lys Lys Glu Gly Ser Ser Pro Lys Glu Asp
240          325         330         335
241      Thr Glu Asp Lys Trp Thr Val Glu Lys Asn Lys Asp His Lys Gly Pro
242          340         345         350
243      Arg Lys Gly Glu Glu Leu Glu Glu Glu Trp Ala Pro Val Glu Lys Ile

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/693,316

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